

(i) APPLICANT: KARIN, MICHAEL
HIBI, MASAHIKO
LIN, ANNING

(ii) TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: FISH & RICHARDSON P.C.
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/444,393
(B) FILING DATE: 19-MAY-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Haile, Ph.D., Lisa A.,
(B) REGISTRATION NUMBER: 38,347
(C) REFERENCE/DOCKET NUMBER: 07257/017002

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (619) 678-5070
(B) TELEFAX: (619) 678-5099

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

It is well known that the q -adic analogue of the Riemann hypothesis is equivalent to the statement that the q -adic zeta function has no zeros on the line $\Re(s) = 1/2$. This is a well-known result in the theory of p -adic numbers.

(vii) IMMEDIATE SOURCE:

(B) CLONE: c-Jun/JNK binding site

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
1 5 10 15

Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
20 25 30

Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTGCAGGAT CCCCATGACT GCAAAGATGG AAACG

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

64

1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as $\epsilon \rightarrow 0$. It is shown that the solutions of the system (1) converge to the solutions of the system (2) as $\epsilon \rightarrow 0$.

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(A) NAME/KEY: CDS
(B) LOCATION: 1..35

TCTGCAGGAT CCCCAAGAAC TCGGACCTCC TCACC

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: C-terminal primer

(A) NAME/KEY: CDS
(B) LOCATION: 1..30

TGAATTCTGC AGGCGCTCCA GCTCGGGCGA

30

CTGTCAAAGG CTCCGGGGGG CGCGGGTGTG CCCCCTTGC CAGAGCCCTG TTGCGGCCCC	360
GAAACTTGTG CGCGCACGCC AAATAACCT CACGTGAAGT GACGGACTGT TCT ATG Met 1	416
ACT GCA AAG ATG GAA ACG ACC TTC TAT GAC GAT GCC CTC AAC GCC TCG Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser 5 10 15	464
TTC CTC CCG TCC GAG AGC GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile 20 25 30	512
CTG AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu 35 40 45	560
AAG CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp 50 55 60 65	608
GTG GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC CTG ATA ATC Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile 70 75 80	656
CAG TCC AGC AAC GGG CAC ATC ACC ACC ACG CCG ACC CCC ACC CAG TTC Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe 85 90 95	704
CTG TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly 100 105 110	752
TTC GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC ACG CTG CCC AGC Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser 115 120 125	800
GTC ACG TCG GCG GCG CAG CCG GTC AAC GGG GCA GGC ATG GTG GCT CCC Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro 130 135 140 145	848
GCG GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC GGC TTC AGC GCC Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala 150 155 160	896
AGC CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn 165 170 175	944
CCA GGC GCG CTG AGC AGC GGC GGC GGG GCG CCC TCC TAC GGC GCG GCC Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala Ala 180 185 190	992

GGC CTG GCC TTT CCC GCG CAA CCC CAG CAG CAG CAG CCG CCG CAC	1040
Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Pro Pro His	
195 200 205	
CAC CTG CCC CAG CAG ATG CCC GTG CAG CAC CCG CGG CTG CAG GCC CTG	1088
His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala Leu	
210 215 220 225	
AAG GAG GAG CCT CAG ACA GTG CCC GAG ATG CCC GGC GAG ACA CCG CCC	1136
Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro Pro	
230 235 240	
CTG TCC CCC ATC GAC ATG GAG TCC CAG GAG CGG ATC AAG GCG GAG AGG	1184
Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg	
245 250 255	
AAG CGC ATG AGG AAC CGC ATC GCT GCC TCC AAG TGC CGA AAA AGG AAG	1232
Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys	
260 265 270	
CTG GAG AGA ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCT	1280
Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala	
275 280 285	
CAG AAC TCG GAG CTG GCG TCC ACG GCC AAC ATG CTC AGG GAA CAG GTG	1328
Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val	
290 295 300 305	
GCA CAG CTT AAA CAG AAA GTC ATG AAC CAC GTT AAC AGT GGG TGC CAA	1376
Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys Gln	
310 315 320	
CTC ATG CTA ACG CAG CAG TTG CAA ACA TTT TGAAGAGAGA CCGTCGGGGG	1426
Leu Met Leu Thr Gln Gln Leu Gln Thr Phe	
325 330	
CTGAGGGGGCA ACGAAGAAAA AAAATAACAC AGAGAGACAG ACTTGAGAAC TTGACAAGTT	1486
GCGACGGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG	1546
GGTTCGGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGGAA GGACTTGGTC GCGCCCTCCC	1606
TTGGCGTGGA GCCAGGGAGC GGCCGCCTGC GGGCTGCCCC GCTTTGCGGA CGGGCTGTCC	1666
CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA	1726
TTCGATCTCA TTCAGTATTA AAGGGGGGAG GGGGAGGGGG TTACAACTG CAATAGAGAC	1786
TGTAGATTGC TTCTGTAGTA CTCCTTAAGA ACACAAAGCG GGGGGAGGGT TGGGGAGGGG	1846
CGGCAGGAGG GAGGTTTGTG AGAGCGAGGC TGAGCCTACA GATGAACCTCT TTCTGGCCTG	1906
CTTTCGTAA CTGTGTATGT ACATATATAT ATTTTAAAT TTGATTAAAG CTGATTACTG	1966

TCAATAAACA GCTTCATGCC TTTGTAAGTT ATTTCTTGTT TGTTTGTTTG GGTATCCTGC 2026
 CCAGTGTGTG TTGTAAATAA GAGATTTGGA GCACTCTGAG TTTACCATTT GTAATAAAGT 2086
 ATATAATTTT TTT 2099

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
 1 5 10 15
 Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
 20 25 30
 Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
 35 40 45
 Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
 50 55 60
 Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
 65 70 75 80
 Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
 85 90 95
 Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
 100 105 110
 Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
 115 120 125
 Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
 130 135 140
 Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
 145 150 155 160
 Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe
 165 170 175
 Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
 180 185 190

SECRET